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SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: WAHL, DR., GEOFFREY M.
O'GORMAN DR., STEPHEN V.
- (ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN
MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL
THEREFOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
(B) STREET: 444 South Flower Street, Suite 2000
(C) CITY: Los Angeles
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 90071
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/666,252
(B) FILING DATE: 08-MAR-1991
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: REITER MR., STEPHEN E.
(B) REGISTRATION NUMBER: 31192
(C) REFERENCE/DOCKET NUMBER: P31 8929
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (619) 535-9001
(B) TELEFAX: (619) 535-8949

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B

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:
 (B) CLONE: NATIVE FLP

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT 48
 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Lys Val Leu Val
 1 5 10 15

CGT CAG TTT GTG GAA AGG TTT GAA AGA CCT TCA GGT GAG AAA ATA GCA 96
 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala
 20 25 30

TTA TGT GCT GCT GAA ACC TAT TTA TGT TGG ATG ATT ACA CAT AAC 144
 Leu Cys Ala Ala Glu Leu Thr Tyr Cys Trp Met Ile Thr His Asn
 35 40 45

GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA 192
 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
 50 55 60

AGC AAT TCG CTG AGT TTC GAT ATT GTC AAT AAA TCA CTC CAG TTT AAA 240
 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
 65 70 75 80

TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAG AAA TTG 288
 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
 85 90 95

ATT CCT GCT TGG GAA TTT ACA ATT ATT CCT TAC TAT GGA CAA AAA CAT 336
 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
 100 105 110

CAA TCT GAT ATC ACT GAT ATT GTA AGT AGT TTG CAA TTA CAG TTC GAA 384
 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
 115 120 125

TCA TCG GAA GAA GCA GAT AAG GGA AAT AGC CAC AGT AAA AAA ATG CTT 432
 Ser Ser Glu Glu Ala Asp Lys Lys Gly Asn Ser His Ser Lys Lys Met Leu
 130 135 140

AAA GCA CTT CTA AGT GAG GGT GAA AGC ATC TGG GAG ATC ACT GAG AAA 480
 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Lys Glu Thr Glu Lys
 145 150 155 160

ATA CTA AAT TCG TTT GAG TAT ACT TCG AGA TTT ACA AAA ACA AAA ACT 528
 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
 165 170 175

TTA Leu	TAC Tyr	CAA Gln	TTC Phe 180	CTC Leu	TTC Phe	CTA Leu	GCT Ala	ACT Thr 185	TTC Phe	ATC Ile	AAT Asn	TGT Cys	GGA Gly 190	AGA Arg	TTC Phe	576
AGC Ser	GAT Asp	ATT Ile 195	AAG Lys	AAC Asn	GTT Val	GAT Asp	CCG Pro 200	AAA Lys	TCA Ser	TTT Phe	AAA Lys	TTA Leu 205	GTC Val	CAA Gln	AAT Asn	624
AAG Lys	TAT Tyr 210	CTG Leu	GGA Gly	GTA Val	ATA Ile 215	ATC Ile 215	CAG Gln	TGT Cys	TTA Leu	GTG Val	ACA Thr 220	GAG Glu	ACA Thr	AAG Lys	ACA Thr	672
AGC Ser 225	GTT Val	ACT Ser	AGG Arg	CAC His	ATA Ile 230	TAC Tyr	TTC Phe	TTT Phe	AGC Ser	GCA Ala 235	AGG Arg	GGT Gly	AGG Arg	ATC Ile	GAT Asp 240	720
CCA Pro	CTT Leu	GTA Val	TAT Tyr	TTG Leu 245	GAT Asp	GAA Glu	TTT Phe	TTG Leu 250	AGG Arg	AAT Asn	TCT Ser	GAA Glu	CCA Val 255	GTC Val	CTA Leu	768
AAA Lys	CGA Arg	GTA Val	AAT Asn 260	AGG Arg	ACC Thr	GGC Gly	AAT Asn	TCT Ser 265	TCA Ser	AGC Ser	AAT Asn	AAA Lys	CAG Gln 270	GAA Glu	TAC Tyr	816
CAA Gln	TTA Leu 275	TTA Leu	AAA Lys	GAT Asp	AAC Asn	TTA Leu 280	GTC Val	AGA Arg	TCG Ser	TAC Tyr	AAT Asn	AAA Lys 285	GCT Ala	TTG Leu	AAG Lys	864
AAA Lys	AAT Asn 290	GCG Pro	CCT Tyr	TAT Ser	TCA Ser	ATC Ile 295	TTT Phe	GCT Ala	ATA Ile	AAA Lys	AAT Asn 300	GGC Gly	CCA Pro	AAA Lys	TCT Ser	912
CAC His 305	ATT Ile	GGA Gly	AGA Arg	CAT His	TTG Leu 310	ATG Met	ACC Thr	TCA Phe	TTT Phe 315	CTT Leu	TCA Met	ATG Met	AAG Lys	GGC Gly	CTA Leu 320	960
ACG Thr	GAG Glu	TTG Leu	ACT Thr	AAT Asn 325	GTT Val	GTG Val	GGA Gly	AAT Asn	TGG Trp 330	AGC Ser	GAT Asp	AAG Lys	CGT Arg 335	GCT Ala	TCT Ser	1008
GCC Ala	GTG Val	GCC Ala	AGG Arg 340	ACA Thr	ACG Thr	TAT Tyr	ACT Thr	CAT His 345	CAG Gln	ATA Ile	ACA Thr	GCA Ala 350	ATA Ile 350	CCT Pro	GAT Asp	1056
CAC His	TAC Tyr	TTC Phe 355	GCA Ala	CTA Leu	GTT Val	TCT Ser	CGG Arg 360	TAC Tyr	TAT Tyr	GCA Ala	TAT Tyr	GAT Asp 365	CCA Pro	GCA Ala	TCA Ser	1104
AAG Lys	GAA Glu 370	ATG Met	ATA Ile	GCA Ala	TTG Leu	AAG Lys 375	GAT Asp	GAG Glu	ACT Thr	AAT Asn	CCA Pro 380	ATT Ile	GAG Glu	GAG Glu	TGG Trp	1152
CAG Gln 385	CAT His	ATA Ile	GAA Glu	CAG Gln	CTA Leu 390	AAG Lys	GGT Gly	AGT Ser	GCT Ala	GAA Glu 395	GGA Gly	AGC Ser	ATA Ile	CGA Arg	TAC Tyr 400	1200
CCC Pro	GCA Ala	TGG Trp	AAT Asn 405	GGG Gly	ATA Ile	ATA Ile	TCA Ser	CAG Gln	GAG Glu 410	GTA Val	CTA Leu	GAC Asp	TAC Tyr	CTT Leu 415	TCA Ser	1248
TCC Ser	TAC Tyr	ATA Ile	AAT Asn 420	AGA Arg	CGC Arg	ATA Ile	TAAGTACGCA	TTTAAGCATA	AACACGCACT							1299

ATGCCGTTCT TCTCATGTAT ATATATATAC AGGCAACACG CAGATATAGG TCGCAGCTGA 1359
ACAGTGAGCT GTATGTGCGC A 1380

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 423 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Gln Phe Asp₅ Ile Leu Cys Lys Thr₁₀ Pro Pro Lys Val Leu Val₁₅
Arg Gln Phe Val Glu Arg Phe Glu Arg₂₅ Pro Ser Gly Glu Lys₃₀ Ile Ala
Leu Cys Ala₃₅ Ala Glu Leu Thr Tyr₄₀ Leu Cys Trp Met Ile₄₅ Thr His Asn
Gly Thr₅₀ Ala Ile Lys Arg Ala₅₅ Thr Phe Met Ser Tyr₆₀ Asn Thr Ile Ile
Ser₆₅ Asn Ser Leu Ser Phe₇₀ Asp Ile Val Asn Lys₇₅ Ser Leu Gln Phe Lys₈₀
Tyr Lys Thr Gln Lys₈₅ Ala Thr Ile Leu Glu₉₀ Ala Ser Leu Lys Lys₉₅ Leu
Ile Pro Ala Trp₁₀₀ Glu Phe Thr Ile Ile₁₀₅ Pro Tyr Tyr Gly Gln Lys His
Gln Ser Asp₁₁₅ Ile Thr Asp Ile Val Ser Ser Leu Gln Leu₁₂₅ Gln Phe Glu
Ser Ser₁₃₀ Glu Glu Ala Asp Lys₁₃₅ Gly Asn Ser His Ser₁₄₀ Lys Lys Met Leu
Lys₁₄₅ Ala Leu Leu Ser Glu₁₅₀ Gly Glu Ser Ile Trp₁₅₅ Glu Ile Thr Glu Lys₁₆₀
Ile Leu Asn Ser Phe₁₆₅ Glu Tyr Thr Ser Arg₁₇₀ Phe Thr Lys Thr Lys₁₇₅ Thr
Leu Tyr Gln Phe₁₈₀ Leu Phe Leu Ala Thr₁₈₅ Phe Ile Asn Cys Gly₁₉₀ Arg Phe
Ser Asp Ile₁₉₅ Lys Asn Val Asp Pro₂₀₀ Lys Ser Phe Lys Leu₂₀₅ Val Gln Asn
Lys Tyr₂₁₀ Leu Gly Val Ile Ile₂₁₅ Gln Cys Leu Val Thr₂₂₀ Glu Thr Lys Thr
Ser Val Ser Arg His Ile₂₃₀ Tyr Phe Phe Ser Ala₂₃₅ Arg Gly Arg Ile Asp₂₄₀
Pro Leu Val Tyr Leu₂₄₅ Asp Glu Phe Leu Arg₂₅₀ Asn Ser Glu Pro Val Lys₂₅₅
Lys Arg Val Asn Arg Thr Gly Asn Ser₂₆₅ Ser Ser Asn Lys Gln Glu Tyr₂₇₀

(2) INFORMATION FOR SEQ ID NO:3:

(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

 (C) INDIVIDUAL ISOLATE: Synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCCCGGGC TACCATGGAG AAGTTCCTAT TCCGAAGTTC CTATTCTCTA GAAAGTATAG
GAACTTCA

60

68

BamH1